

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING

ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/590,457
Source: P&T
Date Processed by STIC: 03/05/2006

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/590,457

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- | | | |
|----|--|--|
| 1 | _____ Wrapped Nucleic
Amino Acids | The number/text at the end of each line “wrapped” down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent “wrapping.” |
| 2 | _____ Invalid Line Length | The rules require that a line not exceed 72 characters in length. This includes white spaces. |
| 3 | _____ Misaligned Amino
Numbering | The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead. |
| 4 | _____ Non-ASCII | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text. |
| 5 | _____ Variable Length | Sequence(s) _____ contain n’s or Xaa’s representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing. |
| 6 | _____ PatentIn 2.0
“bug” | A “bug” in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences. |
| 7 | _____ Skipped Sequences
(OLD RULES) | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where “X” is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where “X” is shown)
This sequence is intentionally skipped
Please also adjust the “(ii) NUMBER OF SEQUENCES:” response to include the skipped sequences. |
| 8 | _____ Skipped Sequences
(NEW RULES) | Sequence(s) _____ missing. If intentional , please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000 |
| 9 | _____ Use of n’s or Xaa’s
(NEW RULES) | Use of n’s and/or Xaa’s have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n’s or Xaa’s are present.
In <220> to <223> section, please explain location of n or Xaa , and which residue n or Xaa represents. |
| 10 | _____ Invalid <213>
Response | <u>Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)</u> |
| 11 | _____ Use of <220> | Sequence(s) _____ missing the <220> “Feature” and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> “Organism” response is “Artificial Sequence” or “Unknown.” Please explain source of genetic material in <220> to <223> section or use “chemically synthesized” as explanation. (See “Federal Register,” 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules |
| 12 | _____ PatentIn 2.0
“bug” | Please do not use “Copy to Disk” function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use “File Manager” or any other manual means to copy file to floppy disk. |
| 13 | _____ Misuse of n/Xaa | “n” can only represent a single nucleotide; “Xaa” can only represent a single amino acid |



PCT

RAW SEQUENCE LISTING

DATE: 09/05/2006

PATENT APPLICATION: US/10/590,457

TIME: 15:11:48

Input Set : E:\Sequence Listing-13987-00020-US.txt

Output Set: N:\CRF4\09052006\J590457.raw

3 <110> APPLICANT: Cirpus, Petra
 4 Bauer, Jorg
 5 Qiu, Xiao
 6 Wu, Guohai
 7 Datla, Nagamani
 9 <120> TITLE OF INVENTION: METHOD FOR PRODUCING POLYUNSATURATED FATTY ACIDS IN
 TRANSGENIC
 10 PLANTS
 12 <130> FILE REFERENCE: 13987-00020-US
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/590,457
 C--> 14 <141> CURRENT FILING DATE: 2006-08-25
 14 <150> PRIOR APPLICATION NUMBER: PCT/EP2005/001863
 15 <151> PRIOR FILING DATE: 2005-02-23
 17 <150> PRIOR APPLICATION NUMBER: DE 10 2004 009 457.8
 18 <151> PRIOR FILING DATE: 2004-02-27
 20 <150> PRIOR APPLICATION NUMBER: DE 10 2004 012 370.5
 21 <151> PRIOR FILING DATE: 2004-03-13
 23 <150> PRIOR APPLICATION NUMBER: DE 10 2004 017 518.7
 24 <151> PRIOR FILING DATE: 2004-04-08
 26 <150> PRIOR APPLICATION NUMBER: DE 10 2004 024 014.0
 27 <151> PRIOR FILING DATE: 2004-05-14
 29 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/07957
 30 <151> PRIOR FILING DATE: 2004-07-16
 32 <150> PRIOR APPLICATION NUMBER: DE 10 2004 062 543.3
 33 <151> PRIOR FILING DATE: 2004-12-24
 35 <160> NUMBER OF SEQ ID NOS: 255
 37 <170> SOFTWARE: PatentIn version 3.3
 40 <210> SEQ ID NO: 1
 41 <211> LENGTH: 1266
 42 <212> TYPE: DNA
 43 <213> ORGANISM: Euglena gracilis
 45 <220> FEATURE:
 46 <221> NAME/KEY: CDS
 47 <222> LOCATION: (1)..(1266)
 48 <223> OTHER INFORMATION: Delta-8 desaturase
 50 <400> SEQUENCE: 1
 51 atg aag tca aag cgc caa gcg ctt ccc ctt aca att gat gga aca aca 48
 52 Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr
 53 1 5 10 15
 56 tat gat gtg tct gcc tgg gtc aat ttc cac cct ggt ggt gcg gaa att 96
 57 Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile
 58 20 25 30
 60 ata gag aat tac caa gga agg gat gcc act gat gcc ttc atg gtt atg 144
 61 Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met

CP9-7)
 Does Not Comply
 Corrected Diskette Needed

CP9-6)

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Input Set : E:\Sequence Listing-13987-00020-US.txt

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62	35	40	45	
64	cac tct caa gaa gcc ttc gac aag ctc aag cgc atg ccc aaa atc aat	192		
65	His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn			
66	50	55	60	
68	ccc agt tct gag ttg cca ccc cag gct gca gtg aat gaa gct caa gag	240		
69	Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu			
70	65	70	75	80
72	gat ttc cgg aag ctc cga gaa gag ttg atc gca act ggc atg ttt gat	288		
73	Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp			
74	85	90	95	
76	gcc tcc ccc ctc tgg tac tca tac aaa atc agc acc aca ctg ggc ctt	336		
77	Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu			
78	100	105	110	
80	gga gtg ctg ggt tat ttc ctg atg gtt cag tat cag atg tat ttc att	384		
81	Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile			
82	115	120	125	
84	ggg gca gtg ttg ctt ggg atg cac tat caa cag atg ggc tgg ctt tct	432		
85	Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser			
86	130	135	140	
89	cat gac att tgc cac cac cag act ttc aag aac cgg aac tgg aac aac	480		
90	His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn			
91	145	150	155	160
93	ctc gtg gga ctg gta ttt ggc aat ggt ctg caa ggt ttt tcc gtg aca	528		
94	Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr			
95	165	170	175	
97	tgc tgg aag gac aga cac aat gca cat cat tcg gca acc aat gtt caa	576		
98	Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln			
99	180	185	190	
101	ggg cac gac cct gat att gac aac ctc ccc ctc tta gcc tgg tct gag	624		
102	Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu			
103	195	200	205	
105	gat gac gtc aca cgg gcg tca cgg att tcc cgc aag ctc att cag ttc	672		
106	Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe			
107	210	215	220	
109	cag cag tat tat ttc ttg gtc atc tgt atc ttg ttg cgg ttc att tgg	720		
110	Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp			
111	225	230	235	240
113	tgt ttc cag agc gtg ttg acc gtg cgc agt ctg aag gac aga gat aac	768		
114	Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn			
115	245	250	255	
117	caa ttc tat cgc tct cag tat aag aag gag gcc att ggc ctc gcc ctg	816		
118	Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu			
119	260	265	270	
122	cat tgg aca ttg aag gcc ctg ttc cac tta ttc ttt atg ccc agc atc	864		
123	His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile			
124	275	280	285	
126	ctc aca tcg ctg ttg gta ttt ttc gtt tcg gag ctg gtt ggc ggc ttc	912		
127	Leu Thr Ser Leu Leu Val Phe Val Ser Glu Leu Val Gly Gly Phe			
128	290	295	300	

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Input Set : E:\Sequence Listing-13987-00020-US.txt

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```

130 ggc att gcg atc gtg gtg ttc atg aac cac tac cca ctg gag aag atc      960
131 Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile
132 305                               310                               315                               320
134 ggg gac tcg gtc tgg gat ggc cat gga ttc tcg gtt ggc cag atc cat      1008
135 Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His
136                               325                               330                               335
138 gag acc atg aac att cgg cga ggg att atc aca gat tgg ttt ttc gga      1056
139 Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly
140                               340                               345                               350
142 ggc ttg aac tac cag atc gag cac cat ttg tgg ccg acc ctc cct cgc      1104
143 Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg
144                               355                               360                               365
146 cac aac ctg aca gcg gtt agc tac cag gtg gaa cag ctg tgc cag aag      1152
147 His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys
148                               370                               375                               380
150 cac aac ctg ccg tat cgg aac ccg ctg ccc cat gaa ggg ttg gtc atc      1200
151 His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile
152 385                               390                               395                               400
155 ctg ctg cgc tat ctg gcg gtg ttc gcc cgg atg gcg gag aag caa ccc      1248
156 Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro
157                               405                               410                               415
159 gcg ggg aag gct cta taa      1266
160 Ala Gly Lys Ala Leu
161                               420
164 <210> SEQ ID NO: 2
166 <211> LENGTH: 421
168 <212> TYPE: PRT
170 <213> ORGANISM: Euglena gracilis
174 <400> SEQUENCE: 2
176 Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr
177 1                               5                               10                               15
180 Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile
181                               20                               25                               30
184 Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met
185                               35                               40                               45
188 His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn
189                               50                               55                               60
192 Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu
193 65                               70                               75                               80
196 Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp
197                               85                               90                               95
200 Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu
201                               100                              105                              110
204 Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile
205                               115                              120                              125
208 Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser
209                               130                              135                              140
212 His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn
213 145                              150                              155                              160

```

RAW SEQUENCE LISTING

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Input Set : E:\Sequence Listing-13987-00020-US.txt

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```

216 Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr
217          165          170          175
220 Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln
221          180          185          190
224 Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu
225          195          200          205
228 Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe
229          210          215          220
232 Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp
233 225          230          235          240
236 Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn
237          245          250          255
240 Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu
241          260          265          270
244 His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile
245          275          280          285
248 Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe
249          290          295          300
252 Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile
253 305          310          315          320
256 Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His
257          325          330          335
260 Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly
261          340          345          350
264 Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg
265          355          360          365
268 His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys
269          370          375          380
272 His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile
273 385          390          395          400
276 Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro
277          405          410          415
280 Ala Gly Lys Ala Leu
281          420
284 <210> SEQ ID NO: 3
286 <211> LENGTH: 777
288 <212> TYPE: DNA
290 <213> ORGANISM: Isochrysis galbana
294 <220> FEATURE:
296 <221> NAME/KEY: CDS
298 <222> LOCATION: (1)..(777)
300 <223> OTHER INFORMATION: Delta-9 elongase
304 <400> SEQUENCE: 3
305 atg gcc ctc gca aac gac gcg gga gag cgc atc tgg gcg gct gtg acc      48
306 Met Ala Leu Ala Asn Asp Ala Gly Glu Arg Ile Trp Ala Ala Val Thr
307 1          5          10          15
309 gac ccg gaa atc ctc att ggc acc ttc tcg tac ttg cta ctc aaa ccg      96
310 Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Lys Pro
311          20          25          30

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```

314 ctg ctc cgc aat tcc ggg ctg gtg gat gag aag aag ggc gca tac agg      144
315 Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg
316          35                      40                      45
318 acg tcc atg atc tgg tac aac gtt ctg ctg gcg ctc ttc tct gcg ctg      192
319 Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu
320          50                      55                      60
322 agc ttc tac gtg acg gcg acc gcc ctc ggc tgg gac tat ggt acg ggc      240
323 Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly
324 65          70                      75                      80
326 gcg tgg ctg cgc agg caa acc ggc gac aca ccg cag ccg ctc ttc cag      288
327 Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln
328          85                      90                      95
330 tgc ccg tcc ccg gtt tgg gac tcg aag ctc ttc aca tgg acc gcc aag      336
331 Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys
332          100                     105                     110
334 gca ttc tat tac tcc aag tac gtg gag tac ctc gac acg gcc tgg ctg      384
335 Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu
336          115                     120                     125
338 agg gtc tcc ttt ctc cag gcc ttc cac cac ttt ggc gcg ccg tgg gat      432
339 Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp
340          130                     135                     140
342 gtg tac ctc ggc att cgg ctg cac aac gag ggc gta tgg atc ttc atg      480
343 Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met
344 145          150                     155                     160
347 ttt ttc aac tcg ttc att cac acc atc atg tac acc tac tac ggc ctc      528
348 Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Leu
349          165                     170                     175
351 acc gcc gcc ggg tat aag ttc aag gcc aag ccg ctc atc acc gcg atg      576
352 Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met
353          180                     185                     190
355 cag atc tgc cag ttc gtg ggc ggc ttc ctg ttg gtc tgg gac tac atc      624
356 Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile
357          195                     200                     205
359 aac gtc ccc tgc ttc aac tcg gac aaa ggg aag ttg ttc agc tgg gct      672
360 Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala
361          210                     215                     220
363 ttc aac tat gca tac gtc ggc tcg gtc ttc ttg ctc ttc tgc cac ttt      720
364 Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe
365 225          230                     235                     240
367 ttc tac cag gac aac ttg gca acg aag aaa tcg gcc aag gcg ggc aag      768
368 Phe Tyr Gln Asp Asn Leu Ala Thr Lys Lys Ser Ala Lys Ala Gly Lys
369          245                     250                     255
371 cag ctc tag      777
372 Gln Leu
376 <210> SEQ ID NO: 4
378 <211> LENGTH: 258
380 <212> TYPE: PRT
382 <213> ORGANISM: Isochrysis galbana
386 <400> SEQUENCE: 4

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<210> SEQ ID NO 115

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Consensus

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<222> LOCATION: (1)..(13)

<223> OTHER INFORMATION: Xaa in the sequence at positions 2, 3, 4, 6, 7, 8 and 9 has the

meaning given in Table A.

<400> SEQUENCE: 115

Asn Xaa Xaa Xaa His Xaa Xaa Met Tyr Xaa Tyr Tyr Xaa
1 10

Invalid Response. 22137 Responses
Can be either Artificial, Unknown
or genus species. See Item 10
on Error Summary sheet.

Insufficient Explanation.
Pls Explain Xaa specifically.

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/590,457

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Input Set : E:\Sequence Listing-13987-00020-US.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:115; Xaa Pos. 2,3,4,6,7,10,13

Seq#:116; Xaa Pos. 3,4,5,6

Seq#:139; Xaa Pos. 3,4

Seq#:140; Xaa Pos. 2,3,5,6

Seq#:141; Xaa Pos. 3

Seq#:142; Xaa Pos. 5,6

Seq#:185; N Pos. 3,18

Seq#:186; N Pos. 3,9,12,15,21

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:121,122,123,124,125,126,127,128,129,130,143,144,145,146,147,148,149,150

Seq#:151,152,153,154,155,156,157,158,159,160,161,162,163,164,165,166,167,168

Seq#:169,170,171,172,173,174,175,176,177,178,179,180,181,182,185,186,187,188

Seq#:189,190,191,192,203,204,205,206,207,208,209,210,211,212,213,214,215,216

Seq#:217,218,219,220,221,222,223,224,225,226,227,228,229,230,231,232,233,234

Seq#:235,236,237,238,239,240,241,242,243,244,245,246,247,248,249,250,251,252

Seq#:253,254,255

VERIFICATION SUMMARY

DATE: 09/05/2006

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Input Set : E:\Sequence Listing-13987-00020-US.txt

Output Set: N:\CRF4\09052006\J590457.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:13227 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:115 after pos.:0

L:13254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:116 after pos.:0

L:14471 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:139 after pos.:0

L:14498 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:140 after pos.:0

L:14525 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:141 after pos.:0

L:14552 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:142 after pos.:0

L:15228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:185 after pos.:0

L:15246 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:186 after pos.:0

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- ☐ **IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**
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- ☐ **BLURRED OR ILLEGIBLE TEXT OR DRAWING**
- ☐ **SKEWED/SLANTED IMAGES**
- ☐ **COLOR OR BLACK AND WHITE PHOTOGRAPHS**
- ☐ **GRAY SCALE DOCUMENTS**
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